

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 13:53:07 ; Search time 117.153 Seconds
(without alignments)
2342.472 Million cell updates/sec

Title: US-09-989-339a-2

Sequence: 1 MASHIVGYPRMGPRLKFA.....ALTMMVSAIKIRIQLASAK 765

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: _geneseqp1980s:*\n2: _geneseqp1990s:*\n3: _geneseqp2000s:*\n4: _geneseqp2001s:*\n5: _geneseqp2002s:*\n6: _geneseqp2003as:*\n7: _geneseqp2003bs:*\n8: _geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3905	100.0	765	ADB23036	Adb23036 Rice meth
2	3697.5	94.7	766	ADA48608	Ada48608 Rice prot
3	3535	90.5	765	ADB23040	ADB23040 Tobacco m
4	3502	89.7	765	ADB23045	ADB23045 Madagasc
5	3472	88.9	765	ABB93994	Abb93994 Hericida
6	3472	88.9	765	ABB93925	Abb93925 Hericida
7	3467	88.8	765	ADB25084	Adb25084 Plant gro
8	3448	88.3	765	AAG53127	Aag53127 Arabidops
9	3448	88.3	765	AAG18607	Aag18607 Arabidops
10	3448	88.3	765	ABB92196	Abb92196 Hericida
11	3395	86.9	763	ADB23038	ADB23038 Soybean m
12	3394	86.9	755	AAG18608	Aag18608 Arabidops
13	3394	86.9	755	AAG53128	Aag53128 Arabidops
14	3357.5	86.0	728	ADA48634	Ada48634 Rice prot
15	3289.5	83.7	768	ADA48100	Ada48100 Rice prot
16	3215	82.3	717	AAG18609	Aag18609 Arabidops
17	3215	82.3	717	AAG53129	Aag53129 Arabidops
18	3194.5	81.8	684	ADA48126	Ada48126 Rice prot
19	3185	81.6	745	AAG27788	Aag27788 Arabidops
20	3131	80.2	735	AAG27789	Aag27789 Arabidops
21	3108.5	79.6	807	ABB93567	Abb93567 Hericida
22	2952	75.6	697	AAG27790	Aag27790 Arabidops
23	2076	53.2	451	ABM73900	Abm73900 DNA clone
24	2060	52.8	446	ABM74475	Abm74475 DNA clone
25	2057.5	52.7	474	AAG39450	Aag39450 Arabidops

26	2003.5	51.3	464	3	AAG39451	Aag39451 Arabidops
27	1833	46.9	758	5	AAU72946	Aau72946 Neisseria
28	1833	46.9	758	5	AAU72999	Aau72999 Neisseria
29	1833	46.9	758	5	AAU72972	Aau72972 Neisseria
30	1824	46.7	758	8	ADP08261	Adp08261 Neisseria
31	1820.5	46.6	426	3	AAG39452	Aag39452 Arabidops
32	1818	46.6	771	6	ABP79516	Abp79516 N. gonorr
33	1776	45.5	768	7	ADP05473	Adp05473 Bacterial
34	1773.5	45.4	794	7	ABO83078	Abob83078 Pseudomon
35	1763	45.1	759	6	ABM68367	Abm68367 Photornab
36	1757.5	45.0	767	8	ADP99011	Adp99011 C. albica
37	1756.5	45.0	760	7	ABO61538	Abob61538 Klebsiell
38	1714	43.9	765	5	ABM48512	Abm48512 Listeria
39	1694.5	43.4	767	7	ADK63384	Adk63384 Disease t
40	1686	43.2	767	5	ABP65725	Abp65725 Bifidobac
41	1674.5	42.9	759	5	ABB54591	Abb54591 Lactococc
42	1673	42.8	749	8	ADK46406	Adk46406 Streptococ
43	1663	42.6	745	5	AAG91007	Aag91007 C. glutami
44	1663	42.6	745	5	AAM51073	Aam51073 Corynebact
45	1660	42.5	749	6	ABU00960	Abu00960 S. pneumo

ALIGNMENTS

RESULT 1	
ADB23036	ADB23036 standard; protein, 765 AA.
XX	
AC	ADB23036;
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Corn methionine synthase.
XX	
KM	enzyme; plant; methionine synthase; methionine; seed; transformed plant;
KW	transgenic; corn.
XX	
OS	Zea mays.
XX	
PN	US2003088886-A1.
XX	
PD	08-MAY-2003.
XX	
PF	28-JAN-2002; 2002US-00989339.
XX	
PR	30-AUG-1995; 95US-0002973P.
XX	
PR	27-AUG-1996; 96US-00703829.
XX	
PR	19-AUG-1999; 99US-00377431.
XX	
PA	(FALC/) FALCO S. C.
XX	
PA	(FAMO/) FAMODU O. O.
XX	
PA	(RAFA/) RAFALSKI J. A.
XX	
PA	(RAMA/) RAMAKER M. L.
XX	
PA	(TARC/) TARCZYNSKI M. C.
XX	
PI	(THOR/) THORPE C.
XX	
PI	Falco SC, Famodu OO, Rafalski JA, Ramaker ML, Tarczyński MC;
XX	Thorpe C;
XX	
DR	WPI; 2003-657990/62.
XX	
DR	N-PSDB; ADB23035.
XX	
PT	New nucleic acid fragments encoding a plant 5-methyltetra-
XX	hydroxyethylglutamate-homocysteine methyl transferase or methionine
XX	synthase, useful for producing increased levels of methionine in the
XX	seeds of transformed plants.
XX	
PS	Example 1; Fig 2; 69pp; English.
XX	
CC	The invention relates to an isolated nucleic acid fragment encoding a
XX	plant methionine synthase. The nucleic acid fragments and chimeric genes
CC	are useful for producing increased levels of methionine in the seeds of

CC transformed plants. The present sequence represents the amino acid
CC sequence of a plant methionine synthase.

XX Sequence 765 AA;

Query Match 100.0%; Score 3905; DB 6; Length 765;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 765; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MASHIVGPRMGKRELKFALESFMDKSSAEDELEKATLDRSISIMQKSEAGIKYIPSN 60
DB 1 MASHIVGPRMGKRELKFALESFMDKSSAEDELEKATLDRSISIMQKSEAGIKYIPSN 60
QY 61 TSSIVYQVLDITMLGAVPERRYSWTGGEIGLSTYFSMARGNATVPAMEMTKWPDYTHFI 120
DB 61 TSSIVYQVLDITMLGAVPERRYSWTGGEIGLSTYFSMARGNATVPAMEMTKWPDYTHFI 120
QY 121 VPBLGPTKFTYASHKAVSEYKEAKALGIDTPVVLGVPVSYLLLSKPAKGVKSFSLSL 180
DB 121 VPBLGPTKFTYASHKAVSEYKEAKALGIDTPVVLGVPVSYLLLSKPAKGVKSFSLSL 180
QY 181 LGSILPIYKEVVAELKAAAGASWIQDEPTLVKDLDAHELAFASSAYALESSFSGLNVL 240
DB 181 LGSILPIYKEVVAELKAAAGASWIQDEPTLVKDLDAHELAFASSAYALESSFSGLNVL 240
QY 241 ETYFADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSPFGSKYLPAGVVDGRNIMA 300
DB 241 ETYFADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSPFGSKYLPAGVVDGRNIMA 300
QY 301 DDLAASLSTLHSLBAVAGKDLVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAQKVE 360
DB 301 DDLAASLSTLHSLBAVAGKDLVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAQKVE 360
QY 361 VNLAKALACOKCEVYFAANAQAASRRSPRTNNEVQKAAALRSDHRSSTTVARL 420
DB 361 VNLAKALACOKCEVYFAANAQAASRRSPRTNNEVQKAAALRSDHRSSTTVARL 420
QY 421 DAOQKLNLPVLPTTTIGSFPOTVELRRVREYKAKITDEYISAIKEISIKVYKIOE 480
DB 421 DAOQKLNLPVLPTTTIGSFPOTVELRRVREYKAKITDEYISAIKEISIKVYKIOE 480
QY 481 LDIDVLVHGEPRNDVYFGEQLSGFAFTANGVQSGRCVCPPIIYGDVSRPNMTV 540
DB 481 LDIDVLVHGEPRNDVYFGEQLSGFAFTANGVQSGRCVCPPIIYGDVSRPNMTV 540
QY 541 FMSKMAQSMTPRPWKMLTGPVTILLMSFVRNDQPRETCYQIALAIKKEVEDELAAGIQ 600
DB 541 FMSKMAQSMTPRPWKMLTGPVTILLMSFVRNDQPRETCYQIALAIKKEVEDELAAGIQ 600
QY 601 VIQIDEAALREGPLRKSEHAFLDMVAHSFRITNCVODTTOHTMCSNFNDIHSI 660
DB 601 VIQIDEAALREGPLRKSEHAFLDMVAHSFRITNCVODTTOHTMCSNFNDIHSI 660
QY 661 IDMDADVITIENSRSDEKLISVREBGVYGAIGPGVYDIHSPIRISTEIRADREKMLA 720
DB 661 IDMDADVITIENSRSDEKLISVREBGVYGAIGPGVYDIHSPIRISTEIRADREKMLA 720
QY 721 VPEPTNLTWNPDCGLKTRKYTEVKPALTNVSAFKLIRTOLASAK 765
DB 721 VPEPTNLTWNPDCGLKTRKYTEVKPALTNVSAFKLIRTOLASAK 765
```

RESULT 2
ADA48608
ID ADA48608 standard; protein; 766 AA.

XX AC ADA48608;

XX DT 20-NOV-2003 (first entry)

DE Rice protein conferring disease resistance in plants.

XX disease resistance; pathogen tolerance; plant pathogen; plant; rice.

XX Oryza sativa.
XX
XX NO2003000906-A2.

XX 03-JAN-2003.

XX 21-JUN-2002; 2002MO-IB002453.

XX 22-JUN-2001; 2001JUS-0300112P.

XX 26-SEP-2001; 2001JUS-0352277P.

XX 22-MAR-2002; 2002JUS-036535P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX GJazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;

XX Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;

XX WPI; 2003-184052/18.

XX N-PSDB; ADA48607.

XX Claim 10; SEQ ID NO 678; 299pp; English.

XX The invention relates to a novel isolated polynucleotide comprising a

XX plant nucleotide sequence having an open reading frame that encodes a

XX polypeptide associated with disease resistance or its fragment having

XX substantially the same activity as the full-length polypeptide. The

XX polynucleotide of the invention is useful for conferring resistance or

XX tolerance to a plant pathogen. The present sequence represents a protein

XX conferring disease resistance used in the invention.

XX Sequence 766 AA;

Query Match 94.7%; Score 3697.5; DB 6; Length 766;
Best Local Similarity 93.5%; Pred. No. 4.4e-301; Indels 1; Gaps 1;
Matches 716; Conservative 28; Mismatches 21;

```
QY 1 MASHIVGPRMGKRELKFALESFMDKSSAEDELEKATLDRSISIMQKSEAGIKYIPSN 60
DB 1 MASHIVGPRMGKRELKFALESFMDKSSAEDELEKATLDRSISIMQKSEAGIKYIPSN 60
QY 61 TSSIVYQVLDITMLGAVPERRYSWTGGEIGLSTYFSMARGNATVPAMEMTKWPDYTHFI 120
DB 61 TSSIVYQVLDITMLGAVPERRYSWTGGEIGLSTYFSMARGNATVPAMEMTKWPDYTHFI 120
QY 121 VPBLGPTKFTYASHKAVSEYKEAKALGIDTPVVLGVPVSYLLLSKPAKGVKSFSLSL 180
DB 121 VPBLGPTKFTYASHKAVSEYKEAKALGIDTPVVLGVPVSYLLLSKPAKGVKSFSLSL 180
QY 181 LGSILPIYKEVVAELKAAAGASWIQDEPTLVKDLDAHELAFASSAYALESSFSGLNVL 240
DB 181 LGSILPIYKEVVAELKAAAGASWIQDEPTLVKDLDAHELAFASSAYALESSFSGLNVL 240
QY 241 ETYFADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSPFGSKYLPAGVVDGRNIM 300
DB 241 ETYFADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSPFGSKYLPAGVVDGRNIM 300
QY 300 ADDLAASLSTLHSLBAVAGKDLVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAQKVE 359
DB 300 ADDLAASLSTLHSLBAVAGKDLVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAQKVE 359
QY 360 EVNALAKALAGOKDEYVFAANAQAASRRSPRTNNEVQKAAALRSDHRSSTTVAR 419
DB 360 EVNALAKALAGOKDEYVFAANAQAASRRSPRTNNEVQKAAALRSDHRSSTTVAR 419
QY 420 LDAOQKLNLPVLPTTTIGSFPOTVELRRVREYKAKITDEYISAIKEISIKVYKIOE 479
DB 420 LDAOQKLNLPVLPTTTIGSFPOTVELRRVREYKAKITDEYISAIKEISIKVYKIOE 479
```

QY 480 ELDIDLVLHGPERNDMEYFGEOLSGFAFTANGVQSGRCVPRPIIYGVSRPNPMT 539
DB 481 ELDIDLVLHGPERNDMEYFGEOLSGFAFTANGVQSGRCVPRPIIYGVSRPNPMT 540
QY 540 VFWSRMAQSMTPRPMKGLTGPVTLNWSFVANDOPRETCYQIALAIKKEVEDLEAGI 599
DB 541 VFWSLAQSMTPRPMKGLTGPVTLNWSFVANDOPRETCYQIALAIKKEVEDLEAGI 600
QY 600 VIOIDEAALREGLEPLRKESEHAFYLDMAVHSFRITNCGVODTTOIHTHMCYSNFDIHS 659
DB 601 VIOIDEAALREGLEPLRKESEHAFYLDMAVHSFRITNCGVODTTOIHTHMCYSNFDIHS 660
QY 660 IIDMDADVITTEINSRDEKLVSFREGVYKAGIGPGVYDIHSPRI PSTEERADRVKML 719
DB 661 IIDMDADVITTEINSRDEKLVSFREGVYKAGIGPGVYDIHSPRI PSTEERADRVKML 720
QY 720 AVFDNITLWVNDGCLKTRKYTEVVPALTNVWSATKLIRTOIASAK 765
DB 721 AVFDNITLWVNDGCLKTRKYTEVVPALTNVWSATKLIRTOIASAK 766

RESULT 3
ADB23040
ID ADB23040 standard; protein; 765 AA.

AC ADB23040;

DT 20-NOV-2003 (first entry)

DE Tobacco methionine synthase.

KW enzyme; plant; methionine synthase; methionine; seed; transformed plant;

KM transgenic; tobacco.

OS Nicotiana tabacum.

PN US200308886-A1.

PD 08-MAY-2003.

PF 28-JAN-2002; 2002US-00989339.

PR 30-AUG-1995; 95US-0002973P.

PR 27-AUG-1996; 96US-00703829.

PR 19-AUG-1999; 99US-00377431.

PA (FALC/) FALCO S C.

PA (FAMO/) FAMODU O O.

PA (RAFA/) RAFALSKI J A.

PA (RAMA/) RAMAKER M L.

PA (TARC/) TARCZYNSKI M C.

PA (THOR/) THORPE C.

PI Falco SC, Famodu OO, Rafalski JA, Ramaker ML, Tarczynski MC,

PI Thorpe C;

DR WPI; 2003-657990/62.

DR N-PSDB; ADB23039.

XX New nucleic acid fragments encoding a plant 5-methyltetra-

XX hydropotereylriglutamate-homocysteine methyl transferase or methionine

XX synthase, useful for producing increased levels of methionine in the

XX seeds of transformed plants.

XX Example 1; Fig 2; 69p; English.

SQL Sequence 765 AA;

Query Match 90.5%; Score 3535; DB 6; Length 765;

Best Local Similarity 88.5%; Pred. No. 2e-287;

Matches 677; Conservative 38; Mismatches 50; Indels 0; Gaps 0;

QY 1 MASHIYGPYRMGPPELKFALSFMDGKSADLEKVTDDRSSIWKOMSEAGIKYIPSN 60
DB 1 MASHIYGPYRMGPPELKFALSFMDGKSADLEKVTDDRSSIWKOMSEAGIKYIPSN 60
QY 61 TSSYYDQVLDITAMGAVPERYSWTGEGISLTFYFSAARGNATVPAMETKMPDTNHYFI 120
DB 61 TSSYYDQVLDITAMGAVPERYSWTGEGISLTFYFSAARGNATVPAMETKMPDTNHYFI 120
QY 121 VPEIGPSTKFTYASHKAVSEYKEAKALCIDVPLVGPVSLLLSKPAKGYEKSPSLSL 180
DB 121 VPEIGPSTKFTYASHKAVSEYKEAKALCIDVPLVGPVSLLLSKPAKGYEKSPSLSL 180
QY 181 LGSILPIYKEVVAELKAAGASWIODEPTLVKODAEHLAFASSAYAELESSFGSLNLYI 240
DB 181 LGSILPIYKEVVAELKAAGASWIODEPTLVKODAEHLAFASSAYAELESSFGSLNLYI 240
QY 241 ETPYADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSPFGKYLPAQVDCRNITWA 300
DB 241 ETPYADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSPFGKYLPAQVDCRNITWA 300
QY 301 DDLAASLSTLHSLBAVAGKDKLVVSTGSLMHTAVDLVNETKLDDEYSMLAFAAQYVE 360
DB 301 DDLAASLSTLHSLBAVAGKDKLVVSTGSLMHTAVDLVNETKLDDEYSMLAFAAQYVE 360
QY 361 VNALAKALAGHGDFAFSANATQAQSKSSPRVTNEAVQKAAALKSGDHRATVSSRL 420
DB 361 VNALAKALAGHGDFAFSANATQAQSKSSPRVTNEAVQKAAALKSGDHRATVSSRL 420
QY 421 DAQCKKMLPVLPTTIGSPQVTELRVREYAKKISEEYKALIKAEIKKVVDIGEE 480
DB 421 DAQCKKMLPVLPTTIGSPQVTELRVREYAKKISEEYKALIKAEIKKVVDIGEE 480
QY 481 LDIDLVLHGPERNDMEYFGEOLSGFAFTANGVQSGRCVPRPIIYGVSRPNPMTV 540
DB 481 LDIDLVLHGPERNDMEYFGEOLSGFAFTANGVQSGRCVPRPIIYGVSRPNPMTV 540
QY 541 FWSKMAQSMTPRPMKGLTGPVTLNWSFVANDOPRETCYQIALAIKKEVEDLEAGIQ 600
DB 541 FWSKMAQSMTPRPMKGLTGPVTLNWSFVANDOPRETCYQIALAIKKEVEDLEAGIQ 600
QY 601 VIOIDEAALREGLEPLRKESEHAFYLDMAVHSFRITNCGVODTTOIHTHMCYSNFDIHSI 660
DB 601 VIOIDEAALREGLEPLRKESEHAFYLDMAVHSFRITNCGVODTTOIHTHMCYSNFDIHSI 660
QY 661 IDMDADVITTEINSRDEKLVSFREGVYKAGIGPGVYDIHSPRI PSTEERADRVKMLA 720
DB 661 IDMDADVITTEINSRDEKLVSFREGVYKAGIGPGVYDIHSPRI PSTEERADRVKMLA 720
QY 721 VFDNITLWVNDGCLKTRKYTEVVPALTNVWSATKLIRTOIASAK 765
DB 721 VFDNITLWVNDGCLKTRKYTEVVPALTNVWSATKLIRTOIASAK 765

RESULT 4
ADB23045
ID ADB23045 standard; protein; 765 AA.

AC ADB23045;

DT 20-NOV-2003 (first entry)

DE Madagascar periwinkle methionine synthase.

KW enzyme; plant; methionine synthase; methionine; seed; transformed plant;

KM transgenic; madagascar periwinkle.

OS Catharanthus roseus.

XX US2003088886-A1.
 XX
 XX
 PD 08-MAY-2003.
 XX
 PF 28-JAN-2002; 2002US-00989339.
 XX
 PR 30-AUG-1995; 95US-0002973P.
 PR 27-AUG-1996; 96US-00703829.
 PR 19-AUG-1999; 99US-00377431.
 XX
 PA (FALC/) FALCO S C.
 PA (FAMO/) FAMODU O O.
 PA (RAFA/) RAFALSKI J A.
 PA (RAMA/) RAMAKER M L.
 PA (TARC/) TARCZYNSKI M C.
 PA (THOR/) THORPE C.
 PI Falco SC, Famodu OO, Rafalski JA, Ramaker ML, Tarczynski MC;
 PI Thorpe C;
 XX
 XX WPI; 2003-657990/62.
 DR
 XX
 XX New nucleic acid fragments encoding a plant 5-methyltetra-
 PT hydroxytryptophan-glutamate-homocysteine methyl transferase or methionine
 PT synthase, useful for producing increased levels of methionine in the
 PT seeds of transformed plants.
 XX
 XX Example 1; Fig 2; 69pp; English.
 PS
 XX
 CC The invention relates to an isolated nucleic acid fragment encoding a
 CC plant methionine synthase. The nucleic acid fragments and chimeric genes
 CC are useful for producing increased levels of methionine in the seeds of
 CC transformed plants. The present sequence represents the amino acid
 CC sequence of a plant methionine synthase.
 CC
 XX Sequence 765 AA;
 SQ

Query Match 89.7%; Score 3502; DB 6; Length 765;
 Best Local Similarity 87.5%; Pred. No. 1,2e-284;
 Matches 66; Conservative 47; Mismatches 49; Indels 0; Gaps 0;

QY 1 MASHIVGPPMGKRELKFALESFMDGSSAEDLEKVAATDLRRSISWKMSEAGIKYIPSN 60
 DB 1 MASHIVGPPMGKRELKFALESFMDGSSAEDLEKVAATDLRRSISWKMADAGIKYIPSN 60
 QY 61 TSSYTOQVDTTAMLGAVPERRYMTGTGELSTYFSMARGNATVPAMEMTKWPDYTHFI 120
 DB 61 TSSYTOQVDTTAMLGAVPERRYMTGTGELSTYFSMARGNATVPAMEMTKWPDYTHFI 120
 QY 121 VPFLGSPSTKFTVAASHKAVSEYKEAKALGIDTPVVLVGPVSYLLSKPAKGVESFSLSL 180
 DB 121 VPFLGSPSTKFTVAASHKAVSEYKEAKALGIDTPVVLVGPVSYLLSKPAKGVESFSLSL 180
 QY 181 LGSILPIYKEVVAELRAAGASWIOLEDEPTLVKDLDAHEHLAFASSAYALESSFGSLNVL 240
 DB 181 LGSILPIYKEVVAELRAAGASWIOLEDEPTLVKDLDAHEHLAFASSAYALESSFGSLNVL 240
 QY 241 EYTFPAIPAESYKTLISLGSVTAYGPDILRGATKLDLIRSSFGSGKTLFPGVVDGRITWA 300
 DB 241 EYTFPAIPAESYKTLISLGSVTAYGPDILRGATKLDLIRSSFGSGKTLFPGVVDGRITWA 300
 QY 301 DDLAASLSTASHLEAVAGKDLVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAKQVVE 360
 DB 301 DDLAASLSTASHLEAVAGKDLVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAKQVVE 360
 QY 361 VNALAKALAGQKDEYFFANAAAQASRRSSPRVTNEBQRAAALRGSDHRRSTTVSARL 420
 DB 361 VNALAKALAGQKDEYFFANAAAQASRRSSPRVTNEBQRAAALRGSDHRRSTTVSARL 420
 QY 421 DAQOKKLNLVLTPTTIGSPQTVELRRVREYKAKKITTDEYISAIKEISKVKIOEE 480
 DB 421 DAQOKKLNLVLTPTTIGSPQTVELRRVREYKAKKITTDEYISAIKEISKVKIOEE 480

QY 481 LDIDVLWGEPEKNDVVEYFGEQLSGFAFTANGWVQSGRCVYKPIIYGDVSRPNMTV 540
 DB 481 LDIDVLWGEPEKNDVVEYFGEQLSGFAFTANGWVQSGRCVYKPIIYGDVSRPNMTV 540
 QY 541 FMSKMAQSMTPRPMKMLTGPVTIILWSTYRNDQPFETCYQIALAIKKEVEBLEAAGIQ 600
 DB 541 FMSQTAQSMTPRPMKMLTGPVTIILWSTYRNDQPFETCYQIALAIKKEVEBLEAAGIN 600
 QY 601 VIOIDEAALREGPLRKSEHAFYLDMAVHSFRITNGQVDTQIHTMCSNPNDIHSI 660
 DB 601 VIOIDEAALREGPLRKSEHAFYLDMAVHSFRITNPLDQTIHTMCSNPNDIHSI 660
 QY 661 IDMDADVTIENSRSDEKLSVFEQVYKAGIGPGVYDIHSRIPSTERIADREKMLA 720
 DB 661 IDMDADVTIENSRSSEKLSVFEQVYKAGIGPGVYDIHSRIPSTERIADRIKMLA 720
 QY 721 VFDTNITLWNPDCGLKTRKTYEYKPAITMNVSTKILRQOLASAK 765
 DB 721 VLDNTILWNPDCGLKTRKTYEYKPAITMNVSTKILRQOLASAK 765

RESULT 5
 ABB93994
 ID ABB93994 standard; protein; 765 AA.
 XX
 AC ABB93994;

DT 31-MAY-2002 (first entry)
 XX
 XX Herbicidally active polypeptide SEQ ID NO 3205.
 DE
 XX
 XX Herbicidal; plant; agriculture; herbicide.
 KM
 XX
 OS Arabidopsis thaliana.

XX WO200210210-A2.
 XX
 PN 07-FEB-2002.
 PD
 XX
 XX 28-AUG-2001; 2001WO-EP009892.
 PF
 XX
 XX 28-AUG-2001; 2001WO-EP009892.
 PR
 XX
 XX (PARB) BAYER AG.

PI Tietjen K, Weidler M;
 XX
 XX WPI; 2002-269010/31.
 DR

PT Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 PT organisms.

PS Claim 5; SEQ ID NO 3205; 261bp + Sequence listing; English.

XX The invention relates to identifying target proteins (ABB90790-ABB94016)
 CC for herbicidally active compounds, comprising aligning and comparing
 CC nucleic acid or amino acid sequences from plant with nucleic acid or
 CC amino acid sequences from non-plant organisms using suitable search
 CC parameters, where plant sequences having an E-value greater by a factor
 CC of 3 than the E-value of most similar non-plant sequences are selected.
 CC The polypeptides or nucleic acids encoding them are useful for
 CC identifying modulators. The identified modulators are useful as
 CC herbicides

XX Sequence 765 AA;

Query Match 88.9%; Score 3472; DB 5; Length 765;
 Best Local Similarity 86.8%; Pred. No. 3.8e-282;
 Matches 66; Conservative 47; Mismatches 54; Indels 0; Gaps 0;

Db 601 VQIDBAALREGPLRKSEHAFYLDMAVHSFRITNCGVDSTQIHTHMCYSHFNDDIHSI 660
QY 661 IDMDADVITTEENSRDEKLSVFEKGVYKAGIGPGVYDIHSRIPSTEBIADRVKMLA 720
Db 661 IDMDADVITTEENSRDEKLSVFEKGVYKAGIGPGVYDIHSRIPSTEBIADRVKMLA 720
QY 721 VEDTNILMVNPDGGLKTRKYTEVKPALTNVNSATKLIIRQLASAK 765
721 VLEONILMVNPDGGLKTRKYTEVKPALKNVDAKLIIRSQLASAK 765
RESULT 7
ADE25084 standard; protein; 765 AA.
ADE25084;
29-JAN-2004 (first entry)
Plant growth associated protein seq id 59.
Plant growth: plant growth trait modulation; Brassicaceae; Arabidopsis;
Brassicaceae; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine;
Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon;
Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus;
Quercus.
Magnoliophyta.
US2003188343-A1.
02-OCT-2003.
07-JAN-2003; 2003US-0033877.
09-JAN-2002; 2002US-0347288P.
(LYNX-) LYNX THERAPEUTICS INC.
Bowen BA, Haudenschild CD, Buckler BS;
WPI; 2003-803305/75.
N-PSDB; ADE25054.
New isolated or recombinant polypeptide for use in modulating a plant
growth trait in a flowering plant e.g. in Arabidopsis, Brassica, Zea, or
Oryza.
Claim 8; SEQ ID NO 59; 81bp; English.
The invention describes an isolated or recombinant polypeptide (I)
comprising a sequence: (a) comprising 1 of 30 sequences (S1), as given in
the specification, or a conservative variant; (b) encoded by 1 of 30
sequences (S2), as given in the specification, or a conservative variant;
(c) encoded by a sequence that hybridises under stringent conditions to
S2; and (d) encoded by a sequence 70 % identical to S2. The expression or
activity of (I) is modulated to modulate a plant growth trait in a
flowering plant, of the family Brassicaceae, preferably in a plant that
is Arabidopsis, Brassica, Zea, Oryza, Triticum, Hordeum, Lolium, Sorghum,
Glycine, Medicago, Helianthus, Lactuca, Beta, Vitis, Solanum,
Lycopersicon, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus,
Pinus, or Quercus. A new method is used to detect genes for a plant
growth trait. This is the amino acid sequence of plant growth associated
protein.
Sequence 765 AA;
Query Match 88.8%; Score 3467; DB 7; Length 765;
Best local Similarity 86.7%; Pred. No. 1e-281;
Matches 663; Conservative 47; Mismatches 55; Indels 0; Gaps 0;
QY 1 MASHIVGPRMGKREIKFALSFWDGKSAEDLEKVAITDLRSISWKQSEAGIKYIPSN 60
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Db 1 MASHIVGPRMGKREIKFALSFWDGKSTAEIDLQKVSADLRSSIMKQNSAAGTKIIPSN 60
QY 61 TSSYQVQVLTDTTAMLGAVBERYSMTGSEIGLSTYFSMAGNATVPAMEMTKWFDYVHF 120
Db 61 TFAHYQVQVLTDTTAMLGAVBERYSMTGSEIGLSTYFSMAGNATVPAMEMTKWFDYVHF 120
QY 121 VPELGPSTKFTTASRAVSBYKAKALGIDTPVLYGPPSYLLSLRPKAVKESFSLSL 180
121 VPELGPSTKFTTASRAVSBYKAKALGIDTPVLYGPPSYLLSLRPKAVKESFSLSL 180
Db 121 VPELGPSTKFTTASRAVSBYKAKALGIDTPVLYGPPSYLLSLRPKAVKESFSLSL 180
QY 181 LGSILPIYKEVVALEKAAASWTQIDEPVLVQDLDAHELAFAFSAAELESSGILNVL 240
181 LKPLIPYKEVITELPAAGATWITQIDEPVLVQDLDAHELAFAFSAAELESSGILNVL 240
Db 181 LKPLIPYKEVITELPAAGATWITQIDEPVLVQDLDAHELAFAFSAAELESSGILNVL 240
QY 241 ETPFADIPAESYKTLTSLGVTAVGFDLIRGAKTLDIRSPFSGKYLPAVVDGGRNVA 300
241 ETPFADIPAESYKTLTSLGVTAVGFDLIRGAKTLDIRSPFSGKYLPAVVDGGRNVA 300
Db 241 ETPFADIPAESYKTLTSLGVTAVGFDLIRGAKTLDIRSPFSGKYLPAVVDGGRNVA 300
QY 301 DDIAASLSTLHSEAVAGKDKLVSTSCSLMHTAVDLVNETKLDDEIKSMILAPAOKVVE 360
301 DDIAASLSTLHSEAVAGKDKLVSTSCSLMHTAVDLVNETKLDDEIKSMILAPAOKVVE 360
Db 301 DDIAASLSTLHSEAVAGKDKLVSTSCSLMHTAVDLVNETKLDDEIKSMILAPAOKVVE 360
QY 361 VNLAKRAGQKDEYFANAAQASRRSPRTNEVQKAAALAGSDHRSSTVSARL 420
361 VNLAKRAGQKDEYFANAAQASRRSPRTNEVQKAAALAGSDHRSSTVSARL 420
Db 361 VNLAKRAGQKDEYFANAAQASRRSPRTNEVQKAAALAGSDHRSSTVSARL 420
QY 421 DAOQKLANLPVLTPTTIGSFPTVELRVRREYKAKKITEDEYISAIKEISKVKVIOEE 480
421 DAOQKLANLPVLTPTTIGSFPTVELRVRREYKAKKITEDEYISAIKEISKVKVIOEE 480
Db 421 DAOQKLANLPVLTPTTIGSFPTVELRVRREYKAKKITEDEYISAIKEISKVKVIOEE 480
QY 481 LDIDVLVHGEPERNDEYFGEOLSGFAFTANGVOSYSGRCYKPPYIGDVSRRPMTY 540
481 LDIDVLVHGEPERNDEYFGEOLSGFAFTANGVOSYSGRCYKPPYIGDVSRRPMTY 540
Db 481 LDIDVLVHGEPERNDEYFGEOLSGFAFTANGVOSYSGRCYKPPYIGDVSRRPMTY 540
QY 541 FWSKMAQSMTPRPMKMLTGPVTIILMWSFRVNDQPRFETCYOIALIKKEVELEAAGIQ 600
541 FWSKMAQSMTPRPMKMLTGPVTIILMWSFRVNDQPRFETCYOIALIKKEVELEAAGIQ 600
Db 541 FWSKMAQSMTPRPMKMLTGPVTIILMWSFRVNDQPRFETCYOIALIKKEVELEAAGIQ 600
QY 601 VQIDBAALREGPLRKSEHAFYLDMAVHSFRITNCGVDSTQIHTHMCYSHFNDDIHSI 660
601 VQIDBAALREGPLRKSEHAFYLDMAVHSFRITNCGVDSTQIHTHMCYSHFNDDIHSI 660
Db 601 VQIDBAALREGPLRKSEHAFYLDMAVHSFRITNCGVDSTQIHTHMCYSHFNDDIHSI 660
QY 661 IDMDADVITTEENSRDEKLSVFEKGVYKAGIGPGVYDIHSRIPSTEBIADRVKMLA 720
661 IDMDADVITTEENSRDEKLSVFEKGVYKAGIGPGVYDIHSRIPSTEBIADRVKMLA 720
Db 661 IDMDADVITTEENSRDEKLSVFEKGVYKAGIGPGVYDIHSRIPSTEBIADRVKMLA 720
QY 721 VEDTNILMVNPDGGLKTRKYTEVKPALTNVNSATKLIIRQLASAK 765
721 VLEONILMVNPDGGLKTRKYTEVKPALKNVDAKLIIRSQLASAK 765
Db 721 VLEONILMVNPDGGLKTRKYTEVKPALKNVDAKLIIRSQLASAK 765
RESULT 8
AAG53127 standard; protein; 765 AA.
AAG53127;
18-OCT-2000 (first entry)
Arabidopsis thaliana protein fragment SEQ ID NO: 67610.
Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
Arabidopsis thaliana.
EP1033405-A2.
06-SEP-2000.
25-FEB-2000; 2000EP-00301439.
XX

PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
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PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
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PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
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PR 01-JUN-1999; 99US-0137222P.
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PR 27-JUL-1999; 99US-0145913P.
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PR 02-AUG-1999; 99US-0146386P.
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PR 20-AUG-1999; 99US-0149929P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
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PR 04-OCT-1999; 9905-0157117P.
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PR 26-OCT-1999; 9905-0161360P.
PR 26-OCT-1999; 9905-0161361P.
PR 28-OCT-1999; 9905-0161920P.
PR 28-OCT-1999; 9905-0161922P.
PR 28-OCT-1999; 9905-0161993P.
PR 29-OCT-1999; 9905-0162142P.

Query Match 88.3%; Score 3448; DB 3; Length 765;
Best Local Similarity 86.4%; Pred. No. 4e-280;
Matches 661; Conservative 46; Mismatches 58; Indels 0; Gaps 0;

QY 1 MASHIVGPRMGPRBELKPALESFMDGSSADELXKATLRSISYMKOMSEAGIKYIPSN 60
DB 1 MASHIVGPRMGPRBELKPALESFMDGSSADDQKVSADLRSDIMQMSAAGIKYIPSN 60
QY 61 TSSYVDQVLDLTMTLGAVERYSWTGEGIGLSTYFSMARGNATVPAMEMTKWPDYTHFI 120
DB 61 TFSHYDQVLDLTMTLGAVERYSWTGEGIGLSTYFSMARGNATVPAMEMTKWPDYTHFI 120
QY 121 VPELGEVSTKTYSHKAVSYKKAALGIDTPVPLVGPVSYLLISKPAKVEKSFLLSL 180
DB 121 VPELGEVSTKTYSHKAVSYKKAALGIDTPVPLVGPVSYLLISKPAKVEKSFLLSL 180
QY 181 LGSILPFYKKEVNAELKAGASWIOLEPTLVKODAEHLAFASSAVALSSPSGLNVL 240
DB 181 LKILIPYKKEVNAELKAGASWIOLEPTLVKODAEHLAFASSAVALSSPSGLNVL 240
QY 241 EYTFADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSPSGKYLFAGVVDGRNIMA 300
DB 241 EYTFADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSPSGKYLFAGVVDGRNIMA 300
QY 301 DDLAASISTHSLAEAVAGKTLVSTSCSLMHTAVDLINETKLDDETKSWLAFAAQVVE 360
DB 301 DDLAASISTHSLAEAVAGKTLVSTSCSLMHTAVDLINETKLDDETKSWLAFAAQVVE 360
QY 361 VMLAALAGOKOKEVYRANAAQAASRRSPRVNTNEVQAAAALRGSDHRRSTYARL 420
DB 361 VMLAALAGOKOKEVYRANAAQAASRRSPRVNTNEVQAAAALRGSDHRRSTYARL 420
QY 421 DAQOKKLNLEVLPTTIGSPOTVELRVRREYAKKITEDEYISAKESISKVKIQEE 480
DB 421 DAQOKKLNLEVLPTTIGSPOTVELRVRREYAKKITEDEYISAKESISKVKIQEE 480
QY 481 LDIDVLVHGPERNDVYFGEOLSGFAFTANGVOSYGRCYKPIIYGDVSRNDPMY 540
DB 481 LDIDVLVHGPERNDVYFGEOLSGFAFTANGVOSYGRCYKPIIYGDVSRNDPMY 540

DB 481 LDIDVLVHGPERNDVYFGEOLSGFAFTANGVOSYGRCYKPIIYGDVSRNDPMY 540
QY 541 FMSKMAQSMTPRPMKMLTGPVTLINMSFVRNDQPRFETCYQIALAIKKEVEDLEAAGIQ 600
DB 541 FMSSTAQSMTKRKMCKMLTGPVTLINMSFVRNDQPRHETCYQIALAIKKEVEDLEKGGIG 600
QY 601 VIQIDBAALREGILPKKSEHAFYLDMAVHSFRITNCGVODTTOIHTHMCYSNNDIHSI 660
DB 601 VIQIDBAALREGILPKKSEHAFYLDMAVHSFRITNCGVODTTOIHTHMCYSNNDIHSI 660
QY 661 IDMDADVITTEHSRSEKLLSVREGVKYAGIGPGVYDIHSRIPSTERIADRVEMULA 720
DB 661 IDMDADVITTEHSRSEKLLSVREGVKYAGIGPGVYDIHSRIPSTERIADRVEMULA 720
QY 721 VFPTNIIWNPDCGLTKRKYTEVKPALTMMVSAATKLIRTOLASAK 765
DB 721 VLEQNTILWNPDCGLTKRKYTEVKPALTMMVSAATKLIRTOLASAK 765
RESULT 9
AAG18607
ID AAG18607 standard; protein; 765 AA.
AC AAG18607;
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 20084.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS
XX
PN EPI033405-A2.
XX
XX 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 9905-0121825P.
PR 05-MAR-1999; 9905-0123180P.
PR 09-MAR-1999; 9905-0123548P.
PR 23-MAR-1999; 9905-0125788P.
PR 25-MAR-1999; 9905-0126264P.
PR 29-MAR-1999; 9905-0126785P.
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PR 06-APR-1999; 9905-0128234P.
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PR 24-MAY-1999; 9905-0135629P.

PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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PR 07-JUN-1999; 99US-0137724P.
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PR 10-JUN-1999; 99US-0138540P.
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PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
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PR 17-JUN-1999; 99US-0139492P.
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PR 18-JUN-1999; 99US-0139460P.
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PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
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PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
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PR 29-JUN-1999; 99US-0140991P.
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PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142802P.
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PR 14-JUL-1999; 99US-0143624P.
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PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144864P.
PR 21-JUL-1999; 99US-0145089P.
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PR 28-OCT-1999; 99US-0161992P.

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PR 29-OCT-1999; 99US-0162142P.

Query Match 88.3%; Score 3448; DB 3; Length 765;

Best Local Similarity 86.4%; Pred. No. 4e-280; Mismatches 58; Indels 0; Gaps 0;

Matches 661; Conservative 46; Mismatches 58; Indels 0; Gaps 0;

QY 1 MASHIVGPRMGKRELKFALESFMDGKSSADELEKATLRSISIMKQMSAGIKYIPSN 60
DB 1 MASHIVGPRMGKRELKFALESFMDGKSSADELQKYSADLRSDIMQMSAGIKYIPSN 60
QY 61 TSSYYDQVLDITAMLGAVPERYSWTGEGISTYFSMARGNATVPAMEMTKWFDYNYHFI 120
DB 61 TFSHYDQVLDITAMLGAVPSRYGFTSGEIGLDYFSGMARGNATVPAMEMTKWFDYNYHYI 120
QY 121 VPELGPSTKFTYASHKAVSEYKAKALGIDTPVTVLGPVSYLLSLKPAKVEKSFLLSL 180
DB 121 VPELGPSTKFTYASHKAVSEYKAKALGIDTPVTVLGPVSYLLSLKPAKVEKSFLLSL 180
QY 181 LGSILPYKEVAVELKAAGASWITQDEPTLVKQDLAEHLAFASSAVAELESSFSGLVLI 240
DB 181 LKPLIPYKEVAVELKAAGASWITQDEPTLVKQDLAEHLAFASSAVAELESSFSGLVLI 240
QY 241 ETTYPADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDIRSSPESGKTLFAGVVDGRNIMA 300
DB 241 ETTYPADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDIRSSPESGKTLFAGVVDGRNIMA 300
QY 301 DDLAASLSTHSLAEVAGKDKLVVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAKQVVE 360
DB 301 DDLAASLSTHSLAEVAGKDKLVVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAKQVVE 360
QY 361 VNALAKALAGQKDEVYFPAANAAQAASRRSPRVTENEVOKAAALRGSDHRSRTTVSARL 420
DB 361 VNALAKALAGQKDEVYFPAANAAQAASRRSPRVTENEVOKAAALRGSDHRSRTTVSARL 420
QY 421 DAOQKLNLPVLPPTTIGSFPTVELRRVREYKAKKITEDEYISAIKEISIKVYKIQEE 480
DB 421 DAOQKLNLPVLPPTTIGSFPTVELRRVREYKAKKITEDEYISAIKEISIKVYKIQEE 480
QY 481 LDDIVLVHGBPERNDWVEYFGEOLSGFAFTANGVQSYGSRCPVPIYGDVSRPKMTV 540
DB 481 LDDIVLVHGBPERNDWVEYFGEOLSGFAFTANGVQSYGSRCPVPIYGDVSRPKMTV 540
QY 541 FMSKMAQSTPRPMKGLTGPVTLLNMSFYRNDOPRETCYQALAIKKEVEDELAAGIQ 600
DB 541 FMSKMAQSTPRPMKGLTGPVTLLNMSFYRNDOPRETCYQALAIKKEVEDELEKGI 600
QY 601 VIOIDEALREGLPLRKSEHAFYLDMAVHSFRITNCGVODTQIHTMCSNFNDIHSI 660
DB 601 VIOIDEALREGLPLRKSEHAFYLDMAVHSFRITNCGVODTQIHTMCSNFNDIHSI 660
QY 661 IDMDADVITTEENSRSDKLSVPEGVKYGAGIGPVYDIHSPIRISTEELARVEKMLA 720
DB 661 IDMDADVITTEENSRSDKLSVPEGVKYGAGIGPVYDIHSPIRISTEELARVEKMLA 720
QY 721 VFDTNILWVNDGCLKTRKYTEVFPALTNNVSAFKLIRTOIASAK 765
DB 721 VFDTNILWVNDGCLKTRKYTEVFPALTNNVSAFKLIRTOIASAK 765

RESULT 10
ABB92196
ID ABB92196 standard; protein; 765 AA.

AC ABB92196;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 1407.

KM Herbicidal; plant; agriculture; herbicide.

XX Arabidopsis thaliana.

XX WO200210210-A2.

XX 07-FEB-2002.

XX 28-AUG-2001; 2001WO-EP009892.

XX 28-AUG-2001; 2001WO-EP009892.

XX (FARB) BAYER AG.

XX Tietjen K, Weidler M;

XX WPI; 2002-269010/31.

PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms.

PS Claim 5; SEQ ID NO 1407; 261pp + Sequence Listing; English.

CC The invention relates to identifying target proteins (ABB90790-ABB94016)
CC for herbicidally active compounds, comprising aligning and comparing
CC nucleic acid or amino acid sequences from plant with nucleic acid or
CC amino acid sequences from non-plant organisms using suitable search
CC parameters, where plant sequences having an E-value greater by a factor
CC of 3 than the E-value of most similar non-plant sequences are selected.
CC The polypeptide or nucleic acids encoding them are useful for
CC identifying modulators. The identified modulators are useful as
CC herbicides

XX Sequence 765 AA;

XX Query Match 88.3%; Score 3448; DB 5; Length 765;

XX Best Local Similarity 86.4%; Pred. No. 4e-280; Mismatches 58; Indels 0; Gaps 0;

Matches 661; Conservative 46; Mismatches 58; Indels 0; Gaps 0;

QY 1 MASHIVGPRMGKRELKFALESFMDGKSSADELEKATLRSISIMKQMSAGIKYIPSN 60
DB 1 MASHIVGPRMGKRELKFALESFMDGKSSADELQKYSADLRSDIMQMSAGIKYIPSN 60
QY 61 TSSYYDQVLDITAMLGAVPERYSWTGEGISTYFSMARGNATVPAMEMTKWFDYNYHFI 120
DB 61 TFSHYDQVLDITAMLGAVPSRYGFTSGEIGLDYFSGMARGNATVPAMEMTKWFDYNYHYI 120
QY 121 VPELGPSTKFTYASHKAVSEYKAKALGIDTPVTVLGPVSYLLSLKPAKVEKSFLLSL 180
DB 121 VPELGPSTKFTYASHKAVSEYKAKALGIDTPVTVLGPVSYLLSLKPAKVEKSFLLSL 180
QY 181 LGSILPYKEVAVELKAAGASWITQDEPTLVKQDLAEHLAFASSAVAELESSFSGLVLI 240
DB 181 LKPLIPYKEVAVELKAAGASWITQDEPTLVKQDLAEHLAFASSAVAELESSFSGLVLI 240
QY 241 ETTYPADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDIRSSPESGKTLFAGVVDGRNIMA 300
DB 241 ETTYPADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDIRSSPESGKTLFAGVVDGRNIMA 300
QY 301 DDLAASLSTHSLAEVAGKDKLVVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAKQVVE 360
DB 301 DDLAASLSTHSLAEVAGKDKLVVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAKQVVE 360
QY 361 VNALAKALAGQKDEVYFPAANAAQAASRRSPRVTENEVOKAAALRGSDHRSRTTVSARL 420
DB 361 VNALAKALAGQKDEVYFPAANAAQAASRRSPRVTENEVOKAAALRGSDHRSRTTVSARL 420
QY 421 DAOQKLNLPVLPPTTIGSFPTVELRRVREYKAKKITEDEYISAIKEISIKVYKIQEE 480
DB 421 DAOQKLNLPVLPPTTIGSFPTVELRRVREYKAKKITEDEYISAIKEISIKVYKIQEE 480
QY 481 LDDIVLVHGBPERNDWVEYFGEOLSGFAFTANGVQSYGSRCPVPIYGDVSRPKMTV 540
DB 481 LDDIVLVHGBPERNDWVEYFGEOLSGFAFTANGVQSYGSRCPVPIYGDVSRPKMTV 540

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QY 541 FMSKMAQSMTPRPMKGMLTGPVTLTNSFVRNDOPRFTCYQIALAIKKEVEDLEAAGIQ 600
DB 541 FMSSTASMTSRPMKGMLTGPVTLTNSFVRNDOPRHTCTQIALAIKDEVEDLEKGGIG 600
QY 601 VIQIDEAALREGPLRKSEHAFYLDMAVHSFRITNCGVQDTQTQIHTHMCYSNPNDIHSI 660
DB 601 VIQIDEAALREGPLRKSEHAFYLDMAVHSFRITNCGVQDTQTQIHTHMCYSNPNDIHSI 660
QY 661 IDMDADVITTENSRDEKLSVFREGVYKYGAGIGPGVYDIHSPIRPTSEIADREKMLA 720
DB 661 IDMDADVITTENSRDEKLSVFREGVYKYGAGIGPGVYDIHSPIRPTSEIADREKMLA 720
QY 721 VFDTNIIWVNPDCGLKTRKYTEVPALTNVVSATKLIIRTOLA 765
DB 721 VLEKNIIWVNPDCGLKTRKYTEVPALTNVVSATKLIIRTOLA 765

RESULT 11
ADB23038
ID ADB23038 standard; protein; 763 AA.
AC ADB23038;
DT 20-NOV-2003 (first entry)
DE Soybean methionine synthase.
KW enzyme; plant; methionine synthase; methionine; seed; transformed plant;
KM transgenic; soybean.
OS Glycine max.
XX US2003088886-A1.
XX 08-MAY-2003.
XX 28-JAN-2002; 2002US-00989339.
XX 30-AUG-1995; 95US-0002973P.
XX 27-AUG-1996; 96US-00703629.
XX 19-AUG-1999; 99US-00377431.
XX (FALC/) FALCO S. C.
XX (FAMO/) FAMODU O. O.
XX (RAFA/) RAFALSKI J. A.
XX (RAMA/) RAMAKER M. L.
XX (TARC/) TARCZYNSKI M. C.
XX (THOR/) THORPE C.
PI Falco SC, Famodu OO, Rafalski JA, Ramaker ML, Tarczynski MC;
PI Thorpe C;
DR WPI; 2003-657990/62.
DR N-PSDB; ADB23037.
XX
XX New nucleic acid fragments encoding a plant 5-methyltetra-
XX hydroxyteroyltryptumate-homocysteine methyl transferase or methionine
XX synthase, useful for producing increased levels of methionine in the
XX seeds of transformed plants.
XX
XX Example 1; Fig 2; 69pp; English.
XX
XX The invention relates to an isolated nucleic acid fragment encoding a
XX plant methionine synthase. The nucleic acid fragments and chimeric genes
XX are useful for producing increased levels of methionine in the seeds of
XX transformed plants. The present sequence represents the amino acid
XX sequence of a plant methionine synthase.
XX
XX Sequence 763 AA;
SQ
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Query Match 86.9%; Score 3395; DB 6; Length 763;
Best Local Similarity 85.4%; Pred. No. 1.1e-275;

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Matches 651; Conservative 46; Mismatches 65; Indels 0; Gaps 0;
QY 1 MASHIVGPRMGPRLKFALESFMDKSSADELXATLDRSITWQMSAGIKYIPSN 60
DB 1 MASHIVGPRMGPRLKFALESFMDKSSADELXATLDRSITWQMSAGIKYIPSN 60
QY 61 TSSYDQVLDTTAMLGAVPERYSWTGEGIGLSTYFSMARGNATVPAMEMTKMPTNYHI 120
DB 61 TSSYDQVLDTTAMLGAVPERYSWTGEGIGLSTYFSMARGNATVPAMEMTKMPTNYHI 120
QY 61 TFSFYDQLDATALGAVPRRYGWTGEGIGLSTYFSMARGNATVPAMEMTKMPTNYHI 120
DB 61 TFSFYDQLDATALGAVPRRYGWTGEGIGLSTYFSMARGNATVPAMEMTKMPTNYHI 120
QY 121 VPEIGPSTKFTYASHKAVSEYKEKALGIDTPVAVPVSYLLISPKAKGVKSFSLISL 180
DB 121 VPEIGPSTKFTYASHKAVSEYKEKALGIDTPVAVPVSYLLISPKAKGVKSFSLISL 180
QY 181 LGSILPTIKYEVNALKAGASWITQDEPTLVKQDAHELAFAAFAVLEBSFSGLVLI 240
DB 181 LGSILPTIKYEVNALKAGASWITQDEPTLVKQDAHELAFAAFAVLEBSFSGLVLI 240
QY 241 ETVFADIPAESYKTLTSGVTAYGFDLIRGAKTLDIRSSFPSGKTLFAGVVDGRNIMA 300
DB 241 ETVFADIPAESYKTLTSGVTAYGFDLIRGAKTLDIRSSFPSGKTLFAGVVDGRNIMA 300
QY 301 DDLAASLSTLSLEAVAKDXLVVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAQKVE 360
DB 301 DDLAASLSTLSLEAVAKDXLVVSTSCSLMHTAVDLVNETKLDDEIKSWLAFAAQKVE 360
QY 361 VNALAKLAGOKDEVTFAAANAQAASRRSPRTVNEVQKAAAALRSDHRRRTTVGARL 420
DB 361 VNALAKLAGOKDEVTFAAANAQAASRRSPRTVNEVQKAAAALRSDHRRRTTVGARL 420
QY 421 DAOOKLNLPLPTTTGSPFQTELRVRVREYKAKITDEVTSAIKESIYKVKLOE 480
DB 421 DAOOKLNLPLPTTTGSPFQTELRVRVREYKAKITDEVTSAIKESIYKVKLOE 480
QY 481 LDIDVLVHGBERNDMEYFGEOLSGFAFTANGVQSGRCVCP11YGDVSRPNMTV 540
DB 481 LDIDVLVHGBERNDMEYFGEOLSGFAFTANGVQSGRCVCP11YGDVSRPNMTV 540
QY 541 FMSKMAQSMTPRPMKGMLTGPVTLTNSFVRNDOPRFTCYQIALAIKKEVEDLEAAGIQ 600
DB 541 FMSKMAQSMTPRPMKGMLTGPVTLTNSFVRNDOPRFTCYQIALAIKKEVEDLEAAGIQ 600
QY 601 VIQIDEAALREGPLRKSEHAFYLDMAVHSFRITNCGVQDTQTQIHTHMCYSNPNDIHSI 660
DB 601 VIQIDEAALREGPLRKSEHAFYLDMAVHSFRITNCGVQDTQTQIHTHMCYSNPNDIHSI 660
QY 661 IDMDADVITTENSRDEKLSVFREGVYKYGAGIGPGVYDIHSPIRPTSEIADREKMLA 720
DB 661 IDMDADVITTENSRDEKLSVFREGVYKYGAGIGPGVYDIHSPIRPTSEIADREKMLA 720
QY 721 VFDTNIIWVNPDCGLKTRKYTEVPALTNVVSATKLIIRTOLA 762
DB 721 VFDTNIIWVNPDCGLKTRKYTEVPALTNVVSATKLIIRTOLA 762

RESULT 12
AAG18608
ID AAG18608 standard; protein; 755 AA.
AC AAG18608;
DT 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 20085.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
XX EPI033405-A2.
XX
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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PR 25-FEB-1999; 99US-0121825P.
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PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
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Query Match 86.9%; Score 3394; DB 3; Length 755;

Best Local Similarity 86.2%; Pred. No. 1,3e-275;
Matches 651; Conservative 46; Mismatches 58; Indels 0; Gaps 0;

QY 11 MGPRLKPELESMFDGSSADLEKVAATDSSIMQMSRAGKYIPSNSTSYVDVLD 70
DB 1 MGPRLKPELESMFDGSSADLEKVAATDSSIMQMSRAGKYIPSNSTSYVDVLD 60
QY 71 TTAMGAVPERYSWTGSEIGLSTYFSMARGNATVPAMEMTKMPTNYHFIYPELGPSYKF 130
DB 61 TTAMGAVPSRYGFTSGEIGLDVYFSMARGNATVPAMEMTKMPTNYHFIYPELGPSYKF 120
QY 131 TYASHKAVSEYKAKALGIDTPVLYGVPVSYLLSKPAGVEXKSPSLISLGSLPIYKE 190
DB 121 SYASHKAVNEKEXKALGVEIVPVLYGVPVSYLLSKLAKGVDSKFDLSTLPIKLPYKE 180
QY 191 VVMEIKKAASWIGLDSEPTLVKLDLDAHELAFFSSAYALESPSGINLVLTITYPADIPAE 250
DB 181 VVMEIKKAASWIGLDSEPTLVKLDLDAHELAFFSSAYALESPSGINLVLTITYPADIPAE 240
QY 251 SYKTLTSLGVTAYGFDLIRGAKTLDIRSGFPGSKYLFAGVNGRNIMADLAASITL 310
DB 241 AYKTLTSLGVTAYGFDLIRGAKTLDIRSGFPGSKYLFAGVNGRNIMADLAASITL 300
QY 311 HSLFAVAGKDLVVSTGCSLMHTAVDLVNETKLDDEIKSWLAFAAQKVEVNALAKALAG 370
DB 301 QSLGCVGKDLVVSTGCSLMHTAVDLVNETKLDDEIKSWLAFAAQKVEVNALAKALAG 360
QY 371 OKDEYVFAANAAASRRSSPRVNEEVOKAAALRGSDHRSSTVSAKRLDAQKNTLP 430
DB 361 QTNSEFTANADALSSRRSSPRVNEEVOKAAALRGSDHRSSTVSAKRLDAQKNTLP 420
QY 431 VLPTTTGSPQVTELRVRREYKAKKITEDEYSIAIKEISIKVYKIQEBLIDIVLVHGE 490
DB 421 ILPTTTGSPQVTELRVRREYKAKKISEEDYKAIKEIKKVVLDIQEBLIDIVLVHGE 480

DB 421 ILPTTTGSPQVTELRVRREYKAKKISEEDYKAIKEIKKVVLDIQEBLIDIVLVHGE 480
QY 491 PERNDMWEYFEGEQLSSGAFTANGVOSYGSVCVPRPIIYGVDSVNPMTVWMSKAOGMT 550
DB 481 PERNDMWEYFEGEQLSSGAFTANGVOSYGSVCVPRPIYGVDSVNPMTVWMSKAOGMT 540
QY 551 PRPKGMLTGCVTLINNSFVANDQPREFTCYQIALAIKKEVEDLEAAGIQYIQAIDEALR 610
DB 541 KRPKGMHTGCVTLINNSFVANDQPREFTCYQIALAIKKEVEDLEKGGIGYIQAIDEALR 600
QY 611 EGLPLRKAESHFYLDMAVHSFRITNGVODTQIHTHMCYSNFNDIHSIIMDADVITI 670
DB 601 EGLPLRKAESHFYLDMAVHSFRITNGVODTQIHTHMCYSNFNDIHSIIMDADVITI 660
QY 671 ENSRSDERKLSVFREGYKYGAGIGPYVDIHSPRIPSTEEIADREVEKMLAFDNIILMVN 730
DB 661 ENSRSDERKLSVFREGYKYGAGIGPYVDIHSPRIPSTDEIADRIINKLAVLEQNIILMVN 720
QY 731 PDGGLKTRKYTEVVPALTNMVSATKLIRTOLASAK 765
DB 721 PDGGLKTRKYTEVVPALKAMVDAKLIRSOIGSAK 755
RESULT 13
AAG53128
ID AAG53128 standard; protein; 755 AA.
AC AAG53128;
XX 18-OCT-2000 (first entry)
DT
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 67611.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
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PR 25-OCT-1999; 99US-0161404P.
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PR 26-OCT-1999; 99US-0161359P.

PR 26-OCT-1999; 99US-0161360P
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PR 28-OCT-1999; 99US-0161920P
PR 28-OCT-1999; 99US-0161922P
PR 28-OCT-1999; 99US-0161933P
PR 29-OCT-1999; 99US-0162142P

Query Match	86.9%;	Score 3394;	DB 3;	Length 755;
Best Local Similarity	86.2%;	Pred. No. 1.3e-275;		
Matches 651;	Conservative 46;	Mismatches 58;	Indels 0;	Gaps 0;

Qy	1	MGKREBELKFLJESFMGKXSADLEKVAADLSSITWKMOSKAGIKYIPSNSSSYDDVD	70
Db	1	MGKREBELKFLJESFMGKXSADLQKNSADLSSDIWKMOSANGIKYIPSNFSHYDDVD	60
Qy	71	TTAMLGAVERYSWMTGGEIGLSTSPSMAGNATVPAMETKMFDTNHYHVPBELGSPSTKF	130
Db	61	TTAMLGAVERYSWMTGGEIGLSTSPSMAGNATVPAMETKMFDTNHYHVPBELGSPSTKF	120
Qy	131	TYASHQAVSEYKEAKRLGIDIVPVLYGVPYSYLLSKPAKYBKSPSLISLGISLIPYKE	190
Db	121	SYASHKAVSEYKEAKRLGIVETPVLYGVPYSYLLSKLAKGVDSFDSLILPKILPYKE	180
Qy	191	VNVELPAAQASWQIDEPFLVMDLDAHELAASAYAELESFSGSLANTLETTYADIPAE	250
Db	181	VNVELPAAQASWQIDEPFLVMDLDBKHQIAQASGAYAELESSTLGLNLTVEYADIPAE	240
Qy	251	SYKTLTSLSGVAYFGDLIRGAKTLIDLRSFSPSGKYFACVVGGRNIMADDLAASLTL	310
Db	241	AYKTLTSLSGVTAFGDVLVRGKTKIDLKSGPQCKYFACVVGGRNIMADDLAASLTL	300
Qy	311	HSLKAVAGDKLVSTSGSLMHTAVDLVNETKLDELKSWLAPAAQKVEYNALAKALAG	370
Db	301	QSLKGVAGDKLVSTSGSLMHTAVDLINETKLDELKSWLAPAAQKVEYDALAKALAG	360
Qy	371	QKQEVYFAANAAQAASRRSPRVTBEOUKAAALARGSDHRRSTTVSARLDAAQCKNLP	430
Db	361	QKQESFFTNADLSSRRSPRVTBESVQKAAALAKGSDHRRSTTVSARLDAAQCKNLP	420
Qy	431	VLPFTTIGSPQTVELRRVRRYKAKKITEDEYISAIKEBISKVYKIQEBLIDIVLVHGE	490
Db	421	ILPFTTIGSPQTVELRRVRRYKAKKISEBYVYKALKEBISKVYVDIQEBLIDIVLVHGE	480
Qy	491	PERNDWVEYFGEOLSGFAFTANGVQSYGSRCKVPEIYGVDSRPNPWTYFWSMAQSMT	550
Db	481	PERNDWVEYFGEOLSGFAFTANGVQSYGSRCKVPEIYGVDSRPNPWTYFWSMAQSMT	540
Qy	551	PRPMKMLGPATLILNWSFVRNDORPEFCVOIALAKKEVEDLEAAGIOYIOIDEALR	610
Db	541	KPRMKMLGPATLILNWSFVRNDORPEHFCYOIALAIDEVEDLEKGGIYIOIDEALR	600
Qy	611	EGLPLRKSEHAFLDWAHVSFRITNCGVODTQIHTHCYGNFNDIHSIITDMADAVYTI	670
Db	601	EGLPLRKASHSYLDWAHVSFRITNCGVODSQIHTHCYGNFNDIHSIITDMADAVYTI	660
Qy	671	ENSRSDKLLSVFREGVKYAGIGCVYDIHSPRIIPSTEEIADREVERKALVFTNTILMVN	730
Db	661	ENSRSEDEKLLSVFREGVKYAGIGCVYDIHSPRIIPSTDEIADRIINKMLAVLEQNILMVN	720
Qy	731	PDCGLKTRKYTEVKPALTNMVSATKLITOTOLASAK	785
Db	721	PDCGLKTRKYTEVKPALKAMDAAKLISQOLGASAK	755

RESULT 14	
AD48634	
ID	AD48634 standard; protein; 728 AA.
XX	
AC	AD48634;
DT	
XX	
XX4	20-NOV-2003 (first entry)
DE	Rice protein conferring disease resistance in plants

KX	disease resistance; pathogen tolerance; plant pathogen; plant; rice.
XX	
OS	Oryza sativa.
PN	WO2003000906-A2.
XX	
PD	03-JAN-2003.
XX	
PF	21-JUN-2002; 2002MO-IB002453.
XX	
PR	22-JUN-2001; 2001US-0300112P.
PR	26-SEP-2001; 2001US-0352277P.
PR	22-MAR-2002; 2002US-0366535P.
PA	(SYGN) SYNGENTA PARTICIPATIONS AG.
XX	
PI	Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T,
PI	Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX	WPI: 2003-184052/18.
DR	N-PDSB; ADA48633.
XX	
PT	New polynucleotide comprising a plant nucleotide sequence having an open
PT	reading frame that encodes a polypeptide associated with disease
PT	resistance, useful for conferring resistance or tolerance to a plant
PT	pathogen.
PS	Claim 10; SEQ ID NO 704; 299pp; English.
XX	
CC	The invention relates to a novel isolated polynucleotide comprising a
CC	plant nucleotide sequence having an open reading frame that encodes a
CC	polypeptide associated with disease resistance or its fragment having
CC	substantially the same activity as the full-length polypeptide. The
CC	polynucleotide of the invention is useful for conferring resistance or
CC	tolerance to a plant pathogen. The present sequence represents a protein
CC	conferring disease resistance used in the invention.
XX	
SQ	Sequence 728 AA:
Query Match	86.0%; Score 3357.5; DB 6; Length 728;
Best Local Similarity	84.5%; Pred. No. 1.5e-272;
Matches 662; Conservative 29; Mismatches 19; Indels 73; Gaps 3	
Dn	1 MASHIVGPRMGPRBELKFALESFMDGSSADELEKVATDTRSSIMKOMSEAGIKYIFSN 60
Dn	1 MASHIVGPRMGPRBELKFALESFMDGSSADELEKVATDTRSSIMKOMADAGITIFSN 60
Dn	61 TTSYYDOVLDTTAMLGAVPERYSWTGBIGLSTYFSMARGNATVPAMEMTKPDTNYHFI 120
Dn	61 TFSYYDDQLDTTAMLGAVPERYSWTGBIGSTYFSMARGNATVPAMEMTKPDTNYHFI 120
Dn	121 VPELGPSTKFTYASHKAVSEYEKAALGIDTPVPLVNGPVSTLLSKPAKGVEKSSLLSL 180
Dn	121 VPELGPSTKFTSYSHHKAVNEYKEKKALGVDPVPLVGVSYLTLISKPAKGVEKSPALLSL 180
Dn	181 LGSILPIFYKEVVAELKKAASGMIOLEDEPLLAKVDHAHELAFFSSAYAELESSFGLANLYI 240
Dn	181 LSSLIPFYKEVVAELKKAAGATWIOPDEPTLVLDSDHQALFAAAYTBESALSGLNVI 240
Dn	241 ETTYPADIPAESYKLTLSISGVTA YGFDLIRSGKTLDLVKSAGFPFGSKYLPAGVVDRNIW 300
Dn	241 ETTYPADIPAESYKLTLSISGVTA YGFDLIRSGKTLDLVKSAGFPFGSKYLPAGVVDRNIW 300
Dn	300 ADDILAASLSTHSLEAVAAGDKLVYSTSCSMTATVNLVNETKDDDELKSLAPAAQKYV 359
Dn	301 ADDILAASLSTHSLEAIVGDKLVYSTSCSMTATVNLVNETKDDSELKSLAPAAQKYV 360
Dn	360 EVNALAALAGQOKE-----VFEAANAQAASRRSPRTNEEVOKAA 402
Dn	361 EVNALAALAGQOKEHLKLLIITYPPNNIVQAFYANTATAQARRRSPRTNEEVOKAA 420
Dn	403 AALGSDHRRTTVSARLDAQOKKLNPVLPTTTIGSFPTVELRVRYREYKAKKIIDE 462

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Db      421 AALRGSDHRRATVNSAFLDAQKKLNPVLPTTIGSPQTVELRRVRRREYKAKKISEDE 480
Qy      463 YISAIRKEISKVVKIOBELIDVLVHGEPRNDVVEFGQSLGFAFTANGWQSVGSR 522
Db      481 YSAIRKEISKVVKIOBELIDVLVHGEPRNDVVEFGQSLGFAFTANGWQSVGSR 538
Qy      523 VKPEIIVGVDSRPNPMTVFWSKMAQSWTPRPMKMLTGPTIILNWSFVRNDQPFETCYQ 582
Db      539 -----RFEICYQ 545
Qy      583 IALAIRKEVVDLEAGIQVIOIDEAALREGLPLRKSEHAFLDMVHSPRITNCGVODTT 642
Db      546 IALAIRKEVVDLEAGIQVIOIDEAALREGLPLRKSEHAFLDMVHSPRITNCGVODTT 605
Qy      643 QIHTMVCYSNFNDIHSIITMDADVITENSRDEKLSVFRSGVKYAGIGGVYDIHS 702
Db      606 QIHTMVCYSNFNDIHSIITMDADVITENSRDEKLSVFRSGVKYAGIGGVYDIHS 665
Qy      703 PRIPSTEEIADRVKMLAVEFDITILMVNPDGGLKTRKYTEVKPALTMVSAATKLIPTOLA 762
Db      666 PRIPSTEEIADRVKMLAVEFDITILMVNPDGGLKTRKYTEVKPALTMVSAATKLIPTOLA 725
Qy      763 SAK 765
Db      726 SAK 728

RESULT 15
ADA48100 ID ADA48100 standard; protein; 768 AA.
XX
AC ADA48100;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice protein conferring disease resistance in plants.
XX
KM disease resistance; pathogen tolerance; plant pathogen; plant; rice.
XX
OS Oryza sativa.
XX
PN WO2003000906-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002MO-IB002453.
XX
PR 22-JUN-2001; 2001US-0300112P.
PR 26-SEP-2001; 2001US-0352277P.
PR 22-MAR-2002; 2002US-0366535P.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX
DR WPI; 2003-184052/18.
DR N-PSDB; ADA48099.
XX
PT New polynucleotide comprising a plant nucleotide sequence having an open
PT reading frame that encodes a polypeptide associated with disease
PT resistance, useful for conferring resistance or tolerance to a plant
PT pathogen.
XX
PS Claim 10; SEQ ID NO 170; 299pp; English.
XX
CC The invention relates to a novel isolated polynucleotide comprising a
CC plant nucleotide sequence having an open reading frame that encodes a
CC polypeptide associated with disease resistance or its fragment having
CC substantially the same activity as the full-length polypeptide. The
CC polynucleotide of the invention is useful for conferring resistance or
CC tolerance to a plant pathogen. The present sequence represents a gene

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CC conferring disease resistance used in the invention.
XX
SQ Sequence 768 AA;
Qy      1 MASHIVGPRMGKRELKFALESFMDGSSAEDELKAVATDLRSISYKQMSSEAGIKYIPSN 60
Db      1 MASHIVGPRMGKRELKFALESFMDGSSAEDELKAVATDLRSISYKQMSSEAGIKYIPSN 60
Qy      61 TSSYYDQVLDITTAAMLGAVBERYSWTGSEIGLSTYSPMAGNATVPAMEKTKMFDITVHFI 120
Db      61 TFSYYDQVLDITTAAMLGAVBERYSWTGSEIGLSTYSPMAGNATVPAMEKTKMFDITVHFI 120
Qy      121 VPFLGPTSTKFTYASHKAVSEYKAKALGIDTVVNVGPPSYLLLSKPACGVESFELSL 180
Db      121 VPFLGPTSTKFTYASHKAVSEYKAKAGVDTVPVLVGPVSYLLLSKPACGVESFELSL 180
Qy      181 LGSILPIYKEVVAELKAGASWITQDEPTLVKDLDAHELAESFSAVALESSFSGLVLI 240
Db      181 LGSILPIYKEVVAELKAGATWQPDPEPTLVLDLSDHQLAFAFAATTELSALGVLVI 240
Qy      241 ETYFADIPABSYKTLTSLSGVTAVGFDLIRGAKTDLIRSS-PPSGKYLPAVVDGRNIW 239
Db      241 ETYFADIPABSYKTLTSLNSVTAVGFDLIRGAKTDLIRKSGAPPSGKYLPAVVDGRNIW 300
Qy      300 ADDLAASLSTHSLBNVAKDKLVSTGSLMHTAADVLENETLDEIKSWLAFAAKRV 359
Db      301 ADDLAASLSTHSLBNVAKDKLVSTGSLMHTAADVLENETLDEIKSWLAFAAKRV 360
Qy      360 EVNALAKALAGQDEEYVPAANAAQAQRSSPRTVEEYQKAAALRGSDHRRSTVTSAR 419
Db      361 EVNALAKALAGQDEEYVPAANAAQAQRSSPRTVEEYQKAAALRGSDHRRATVTSAR 420
Qy      420 LDAQOKKMLPVLPTTIGSPQTVELRRVRRREYKAKKITEDEYISAIKEISKVKIOE 479
Db      421 LDAQOKKMLPVLPTTIGSPQTVELRRVRRREYKAKKISEEYISAIKEISKVKIOE 480
Qy      480 ELDIDVLVHGEPRNDVVEFGQSLGFAFTANGWQSVGRVCRPIIYGVDSRNPMT 539
Db      481 ELDIDVLVHGEPRNDVVEFGQSLGFAFTANGWQSVGRVCRPIIYGVDSRNPMT 540
Qy      540 VFWSKMAQSWTPRPMKMLTGPTIILNWSFVRNDQ-RFETCYQIALAIKEVEDLEAG 598
Db      541 XXXXXXXXXXXXXMGMLTGPTIILNWSFVRNDQXRFETCYQIALAIKEVEDLEAG 600
Qy      599 IQVIOIDEAALREGLPLRKSEHAFLDMVHSPRITNCGVODTT-QIHTMVCYSNFNDI 657
Db      601 IQVIOIDEAALREGLPLRKSEHAFLDMVHSPRITNCGVODTTQIHTMVCYSNFNDI 660
Qy      658 HSIITMDADVITENSRDEKLSVFRSGVKYAGIGGVYDIHSRISTEEIADRVK 717
Db      661 HSIITMDADVITENSRDEKLSVFRSGVKYAGIGGVYDIHSRISTEEIADRVK 720
Qy      718 MLAVPDTNIIIMVNPDCGLKTRKYTEVKPALTMVSAATKLIPTOLASAK 765
Db      721 MLAVPDTNIIIMVNPDCGLKTRKYTEVKPALTMVSAATKLIPTOLASAK 768

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Search completed: January 3, 2005, 14:08:42
 Job time : 123.153 secs